





Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC2&t=RC2-BN0332-200600-011-d1&t3=2000-06-20&t4=1>)  
Seq primer: puc 18 forward  
High quality sequence start: 13  
High quality sequence stop: 671.

## FEATURES

source

Location/Qualifiers  
1..674

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="BN0332"

/dev\_stage="Adult"

/note="Organ: breast\_normal; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 159 a 166 c 189 g 160 t

## ORIGIN

Query Match 56.5%; Score 92.6; DB 14; Length 674;  
Best Local Similarity 73.0%; Pred. No. 2,3e-17;  
Matches 119; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 2 CACCGGACATCAAGGAGAAATATTTGCTACTGTGAGAAATAGAACATGATGACATC 61

Db 384 CACCGGACCTTAAGTCACAGACATATGATCTCCAGAAAGTGAGATGAGACCTTG 443

QY 62 TGCATTAACCTTGAAGATTACAGATTTGGTGGCGGAGGAATGGCAGACACAC 121

Db 444 AGCAGCAAGATTCTGGAATGACTGATTTGGCTGGCGGAGATGGCAGAACACAC 503

QY 122 AAATGAGACAGACGACCTATGCTGATGGCCGCCAGAG 164

Db 504 AAGATGAGTGGCGGAGGAGCTATGCTTGATGGCACCAGAG 546

RESULT 4  
CNS01VLM 1040 bp DNA linear GSS 12-MAY-2000  
LOCUS Tetradon nigroviridis genome survey sequence pUC-ori end of clone 198N22 of library G from Tetradon nigroviridis, genomic survey sequence.

ACCESSION AL169302.1 GI:7807359

VERSION GSS: genome survey sequence.

KEYWORDS Tetradon nigroviridis.

SOURCE Tetradon nigroviridis.

ORGANISM Tetradon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetradon.

REFERENCE 1 (bases 1 to 1040)  
Roest-Crolius H., Jallion O., Dasilva C., Bouneau L., Fisher C., Bernot A., Fizames C., Wincker P., Brotilier P., Queller F., Saurin W. and Weissenbach J.

REFERENCE 2 (bases 1 to 1040)  
Roest-Crolius H., Jallion O., Dasilva C., Fizames C., Fisher C., Bouneau L., Billault A., Queller F., Saurin W., Bernot A. and Weissenbach J.

REFERENCE 3 (bases 1 to 1040)  
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigroviridis

REFERENCE 4 (bases 1 to 1040)  
Unpublished

REFERENCE 5 (bases 1 to 1040)  
Unpublished

REFERENCE 6 (bases 1 to 1040)  
Unpublished

REFERENCE 7 (bases 1 to 1040)  
Unpublished

REFERENCE 8 (bases 1 to 1040)  
Unpublished

REFERENCE 9 (bases 1 to 1040)  
Unpublished

REFERENCE 10 (bases 1 to 1040)  
Unpublished

REFERENCE 11 (bases 1 to 1040)  
Unpublished

REFERENCE 12 (bases 1 to 1040)  
Unpublished

JOURNAL Submitted (12-APR-2000)  
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetradon>.

## FEATURES

source

Location/Qualifiers  
1..1040

/organism="Tetradon nigroviridis"

/db\_xref="taxon:99883"

/clone\_lib="G"

/note="Genoscope sequence ID : C0AG198DG11SP1-end : PUC-ori"

BASE COUNT 218 a 294 c 290 g 224 t 14 others

## ORIGIN

Query Match 54.6%; Score 89.6; DB 17; Length 1040;  
Best Local Similarity 77.5%; Pred. No. 2.1e-16;  
Matches 107; Conservative 1; Mismatches 30; Indels 0; Gaps 0;

QY 27 TTTTGCTACTTGAGAGATGAGATGATGACATCTGCATTAACCTTTGAAGATTACAG 86

Db 87 TTTTGCTACTTGAGAGATGAGATGATGACATCTGCATTAACCTTTGAAGATTACAG 146

QY 87 ATTTGGGCTTGGCGAGGAGATGGCAGACGACCAAAATGAGCAGCAGCAGCTATG 146

Db 147 ATTTGGGCTTGGCGAGGAGATGGCAGACGACCAAAATGAGCAGCAGCAGCTATG 206

QY 147 CCTGATGGCCCGCAGAG 164

Db 207 CCTGATGGCCCGCAGAG 224

RESULT 5  
CNS0202Z 849 bp DNA linear GSS 15-MAY-2000  
LOCUS Tetradon nigroviridis genome survey sequence T7 end of clone 166022 of library G from Tetradon nigroviridis, genomic survey sequence.

ACCESSION AL213956.1 GI:7872775

VERSION GSS: genome survey sequence.

KEYWORDS Tetradon nigroviridis.

SOURCE Tetradon nigroviridis.

ORGANISM Tetradon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetradon.

REFERENCE 1 (bases 1 to 849)  
Roest-Crolius H., Jallion O., Dasilva C., Bouneau L., Fisher C., Bernot A., Fizames C., Wincker P., Brotilier P., Queller F., Saurin W. and Weissenbach J.

REFERENCE 2 (bases 1 to 849)  
Roest-Crolius H., Jallion O., Dasilva C., Fizames C., Fisher C., Bouneau L., Billault A., Queller F., Saurin W., Bernot A. and Weissenbach J.

REFERENCE 3 (bases 1 to 849)  
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigroviridis

REFERENCE 4 (bases 1 to 849)  
Unpublished

REFERENCE 5 (bases 1 to 849)  
Unpublished

REFERENCE 6 (bases 1 to 849)  
Unpublished

REFERENCE 7 (bases 1 to 849)  
Unpublished

REFERENCE 8 (bases 1 to 849)  
Unpublished

REFERENCE 9 (bases 1 to 849)  
Unpublished

REFERENCE 10 (bases 1 to 849)  
Unpublished

REFERENCE 11 (bases 1 to 849)  
Unpublished

REFERENCE 12 (bases 1 to 849)  
Unpublished

REFERENCE 13 (bases 1 to 849)  
Unpublished

REFERENCE 14 (bases 1 to 849)  
Unpublished

REFERENCE 15 (bases 1 to 849)  
Unpublished

REFERENCE 16 (bases 1 to 849)  
Unpublished

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/db_xref="taxon:99883"
/clone="166022"
/clone_1b="G"
/note="Genoscope sequence ID : COAG166BH11LP1-end : T7
BASE COUNT      169 a      219 c      221 g      216 t      24 others
ORIGIN

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| Query Match               | 53.7% | Score 88;        | DB 17;  | Length 849; |
| Best Local Similarity     | 74.6% | Pred. No. 6e-16; |         |             |
| Matches 103; Conservative | 5;    | Mismatches 0;    | Gaps 0; |             |

```

27  TTTTGCACCTTGAGAAGATAGACATGATGCACATCGCAATAAACTTGAAGATTACAG  86
    ||||| ||||| | ||| | ||||| | : | : ||||| || |
Db  179  TTTTGTTACTTGAAAGGATCGAGAATGAMGCATCGGGAGGAGRAGAMTTGAAGATCACCG  238

```

**Oy**    87 ATTTTGGGTTGGCGAGGGAAATGGCACACGACCACCAAAATGAGCACAGCAGGCACCTATG 146  
       ||||| ||| ||||| ||||| ||||| | : : ||||| |||    - : ||||| ||||  
**Db**    239 ATTTCGGGCTIGGCCAGGAGTGCCACA AAA MMACCAAGATGTGGCTGMAGGCACCTACT 298

|    |     |   |                    |     |
|----|-----|---|--------------------|-----|
| QY | 14  | / | CCTGGATGGCCCCAGAG  | 164 |
|    |     |   |                    |     |
| Db | 299 |   | CCTGGATGGCCCCCTGAG | 316 |

|            |  |        |      |        |                 |
|------------|--|--------|------|--------|-----------------|
| LOCUS      | AM658260   | 486 bp | mRNA | linear | EST 25-APR-2001 |
| DEFINITION | 9A142 MARC 1BOV Bos taurus cDNA 5', mRNA sequence. |        |      |        |                 |
| ACCESSION  | AM658260   |        |      |        |                 |
| RESULT 6   |  |        |      |        |                 |

|          |            |            |
|----------|------------|------------|
| VERSION  | AM658260.1 | GI:7424086 |
| KEYWORDS | EST.       |            |
| SOURCE   | CCW.       |            |

REFERENCE  
AUTHORS  
Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T.,  
1 (pages 1 to 486)  
Bovidae: Bovinae: Bos.  
Eumariyota; Metazoa; Chordata; Craniata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea.  
Bovidae: Bovinae: Bos.

| TITLE  | JOURNAL | GENOME RES. | 11 (4) | 626-630 (2001) |
|--|---------|-------------|--------|----------------|
| Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle |         |             |        |                |

USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel.: 402 763 4366

Email: smith@emmail.marc.usda.gov  
Single pass sequencing. Bases called and alt-trimmed with phred  
v0.9609094.e. Vector identified by cross\_match with the -mismatch 18  
and -mismatch 12 options.

FORWARD: AGGAACACGCTATGACCAT  
 BACKWARD: GTTTTCCCAGTCACGACG  
 Plate: 60 row: N column: 23  
 Seq primer: ATTAGGTGACACTATAG

FEATURES  
SOURCE

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/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1B0V"
/tissue_type="pooled"
/lab_host="Intron"

```

| BASE COUNT | ORIGIN   |
|------------|----------|
| 89 a       | 155 c    |
|            | 140 g    |
|            | 101 t    |
|            | 1 others |

|                           |        |                    |           |             |
|---------------------------|--------|--------------------|-----------|-------------|
| Query Match               | 51.6%; | Score 84.6;        | DB 10;    | Length 486; |
| Best Local Similarity     | 69.9%; | Pred. No. 5.3e-15; |           |             |
| Matches 114; Conservative | 0;     | Mismatches 49;     | Indels 0; | Gaps 0;     |

2 CACCGGGCATCAAGGCCAGGAATATTCTGACTTGAGAAGCTAGAACATGATGCATC 61  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
120 CACCGAAGCTCAAGTCCAACAACATCTTCGTCTGCTGACGCCCATTTGAAGCTGACGCATG 179

62 TGCATTAACCTTGAAGATTACAGATTTTGGTGTGGCGAGGGAATGGCACAGGACCAC 121  
 180 GAGCACAGACCCCTGAAGATCAGGACTTGGGTGTGGCCCGTAGTGGCACAAAAACACG 239

122 A A A T G A G C A C A G C A G G C A C C T A T G C T G A T G G C C C A G A G 164  
||||| - - ||||| ||||| ||||| |||||  
240 C A A T G A G T C T G C G G G C A C C T A T G C C T G G A T G G C T C C T G A G G 282

|                 |        |      |        |   |
|-----------------|--------|------|--------|---|
| EST 25-APR-2001 | linear | mRNA | 551 bp | BE682782  |
|                 |        |      |        | 181081 MARC 4BOV Bos taurus cDNA 5', mRNA sequence. |
|                 |        |      |        | BE682782  |
|                 |        |      |        | DEFINITION  |
|                 |        |      |        | OCUS  |
|                 |        |      |        | SOURCE  |
|                 |        |      |        | ESLUT 7   |
|                 |        |      |        | 6882782   |

## ORGANISM

REFERENCE  
1 (bases 1 to 551)  
Smith T.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,  
Grose, P. W., T. P. L. Smith, B. A. Freking, A. J. Roberts, R. T. Stone, P. W. Grose

| TITLE     | SEQUENCE EVALUATION OF FOUR POOLED-TISSUE NORMALIZED BOVINE CDNA LIBRARIES AND CONSTRUCTION OF A GENE INDEX FOR CATTLE |
|-----------|--|
| JOURNAL   | Genome Res. 11 (4), 626-630 (2001)   |
| EDIT TIME | 21190012   |

**MEDLINE** 21180013  
**COMMENT** Contact: Smith TPL

Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and alt\_trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -mismatch 12 options.  
PCR Primers

FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCCACTCAGCAGC  
Plate: 76 row: M column: 8  
Seq primer: ATTTAGGTGACACTATAG

| source  | Location/Qualifiers |
|---------|---------------------|
| 1. .551 |                     |

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/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 4BOY"
/issue_type="pooled"
/lab_host="murine"

```

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|----------|-------|-------|-------|-------|
| SE COUNT | 106 a | 169 c | 173 g | 103 t |
| IGIN     |       |       |       |       |

|                       |                 |                    |           |             |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match           | 51.6%;          | Score 84.6;        | DB 10;    | Length 551; |
| Best Local Similarity | 69.9%;          | Pred. No. 5.5e-15; |           |             |
| Matches 114;          | Conservative 0; | Mismatches 49;     | Indels 0; | Gaps 0;     |

2 CACCGGACATCAAGGCAGGAATAATTTTGTACTTGAGAAGATAGAACATGATGACATC 61  
||||| ||| ||||| | ||||| ||||| ||| ||||| |||||  
309 CACCGAGACCTCAAGTCACAACACATTTCTGCTGCTGCAGCCCCCATTTGAAAGGTGACCGCATG 368

|  |                 |  |             |
|--|-----------------|--|-------------|
| QY   | 62              | TGCATTAATAACTTTGAGATTTACAGATTTTGTTGGCGAGGAGATGCACAGACACC     | 121         |
| Db   | 369             | GAGCACAAGACCCTGMAAGATACGAGACTTGGTCTGGCCCTGAGTGGCACAAAACACG   | 428         |
| QY   | 122             | AAATGAGCAGCAGCAGCAGCAGCCTATGCTGATGGCCCCAGAAAG                | 164         |
| Db   | 429             | CAATGAGTGTCTGGCGGCACCTATGCTGATGGCTCTCTGAGG                   | 471         |
| RESULT 8   |                 |  |             |
| BQ604135/c   |                 |  |             |
| LOCUS  |                 |  |             |
| DEFINITION   |                 |  |             |
| ACCESSION  |                 |  |             |
| VERSION  |                 |  |             |
| KEYWORDS   |                 |  |             |
| SOURCE   |                 |  |             |
| ORGANISM   |                 |  |             |
| REFERENCE  |                 |  |             |
| AUTHORS  |                 |  |             |
| TITLE  |                 |  |             |
| JOURNAL  |                 |  |             |
| MEDLINE  |                 |  |             |
| COMMENT  |                 |  |             |
| FEATURES   |                 |  |             |
| source   |                 |  |             |
| location/Qualifiers  |                 |  |             |
| 1..791   |                 |  |             |
| /organism="Sus scrofa"   |                 |  |             |
| /strain="crossbred"  |                 |  |             |
| /db_xref="taxon:9823"  |                 |  |             |
| /clone="MI-P-CPI-nzb-a-19-0-UI"  |                 |  |             |
| /clone_lib="MI-P-CPI"  |                 |  |             |
| /lab_host="DH10B (Life Technologies)"  |                 |  |             |
| /note="Vector: pRT3D-Pot (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: EcoRI. The MI-P-CPI library is normalized library derived from uterus tissue. For a detailed description of the library from which this clone was derived, please visit our web site at http://piglet.genome.iastate.edu/. The procedure used to create this library has been previously described (Bonaldo et al., Lennon and Soares, Genome Research 6: 791-806, 1996) TAG-SBO=None found" |                 |  |             |
| BASE COUNT   | 143 a           | 251 c  | 246 g       |
| ORIGIN   |                 |  |             |
| Query Match  | 51.6%           | Score 84.6:  | DB 14;      |
| Best Local Similarity  | 69.9%           | Pred. No. 6.2e-15;   | Length 791; |
| Matches 114;   | Conservative 0; | Mismatches 49;   | Indels 0;   |
| Gaps 0;  |                 |  |             |
| QY   | 2               | CACCGGACATCAACGCGCGAAATTTTGTCTACTTGAAGATGAGCATGATGCATC       | 61          |
| Db   | 694             | CACGAGACCTCAAGTCCACACACACTTCTGCTGCTGACGACCCATGGAAGGTGACACATG | 635         |
| QY   | 62              | TGCATTAATAACTTTGAGATTTACAGATTTTGTTGGCGAGGAGATGCACAGACACC     | 121         |

|                           |                   |   |   |
|---------------------------|-------------------|---|---|
| Db                        | 634               | GAGCACAAGACCCCTGAAGATCATCGACTTGGCGCCGCGCCGAGGTGCACAAAAACGAG     | 575   |
| QY                        | 122               | AAAATGAGCACAGCAGCACCATTATGCTTGATGGCCCCAGAAAG                    | 164   |
| Db                        | 574               | CAAATGAGTCTCGCGGCGACCTATGCCGTCGATGAGCTCTGAGG                    | 532   |
| RESULT 9                  |                   |   |   |
| AU125482                  |                   |   |   |
| LOCUS                     |                   |   |   |
| DEFINITION                |                   |   |   |
| ACCESSION                 | AU125482          | NF2RM4  | Homo sapiens cDNA clone NF2RM4001663 5', mRNA |
| VERSION                   | AU125482.1        |   |   |
| KEYWORDS                  |                   |   |   |
| SOURCE                    |                   |   |   |
| ORGANISM                  |                   |   |   |
| TITLE                     |                   |   |   |
| JOURNAL                   |                   |   |   |
| COMMENT                   |                   |   |   |
| REFERENCE                 |                   |   |   |
| AUTHORS                   |                   |   |   |
| FEATURES                  |                   |   |   |
| ORIGIN                    |                   |   |   |
| BASE COUNT                |                   |   |   |
| Query Match               |                   |   |   |
| Best Local Similarity     | 69.3%             | Pred. No. 1.8e-14;  |   |
| Matches 113; Conservative | 0;                | Mismatches 50;  | Indels 0;                                     |
| DB                        | 2                 | CACCGGACATCAAGCAGCAATAATTTTGGCTACTTGAAGAATGAAACATGATGACATC      | 61  |
| Db                        | 78                | CACGCTGATCTCAAGTCCACACACATTTTGGCTGCTGCAGCCCATGAGAGTAGACACATG    | 137   |
| QY                        | 62                | TGCAATTAACCTTTGAGACATTTACAGATTTTGGGTTGGCGAGGAGAAATGGCACAGCACACC | 121   |
| Db                        | 138               | GAGCACAAGACCCCTGAAGATCATCGACTTGGCGCCGCGGAGGTGCACAAAAACGAG       | 197   |
| QY                        | 122               | AAAATGAGCACAGCAGCACCATTATGCTTGATGGCCCCAGAAAG                    | 164   |
| Db                        | 198               | CAAATGAGTCTCGCGGCGACCTATGCCGTCGATGAGCTCTGAGG                    | 240   |
| RESULT 10                 |                   |   |   |
| LOCUS                     |                   |   |   |
| DEFINITION                |                   |   |   |
| ACCESSION                 | BQ719600          | 873 bp  | mRNA linear EST 16-JUL-2002                   |
| LOCUS                     |                   |   |   |
| DEFINITION                |                   |   |   |
| ACCESSION                 | AGNCOCURT_8234446 | lupski_sympathetic_trunk Homo sapiens cDNA clone                |   |

IMAGE:618692.5', mRNA sequence.  
ACCESSION BQ719600  
VERSION BQ719600.1 GI:21858497  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 873)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Dr. James R. Lupski  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM13584 row: 1 column: 05  
High quality sequence stop: 620.  
FEATURES  
source  
Location/Qualifiers  
1. 873  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:618692"  
/clone\_lib="Lupski\_sympathetic\_trunk"  
/sex="male"  
/tissue\_type="sympathetic trunk"  
/dev\_stage="adult, 16 yr"  
/lab\_host="DH10B"  
/note="Vector: PCMV-SPORT6 (Life Technologies); Site\_1: NotI; Site\_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTCTAGATCGGAGCGGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."  
BASE COUNT 167 a 271 c 270 g 165 t  
ORIGIN  
Query Match 50.6%; Score 83; DB 14; Length 873;  
Best Local Similarity 69.3%; Pred. No. 1.9e-14;  
Matches 113; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
QY 2 CACCGGACATCAAGCAGGAATATTTGCTCTGAGAAGATGACATGACATC 61  
DB 376 CACCGGATCTCAAGTCCAAACATTTTCTCTGAGCCCATTTGAGATGACGACATG 435  
QY 62 TGCATATAAACTTTGAAGATTACAGATTTTGGTTGGCGAGGAGATGACAGACAC 121  
DB 436 GACGACAAAGACCTGAAGATCACGCACTTGGCTGGCCCGAAGTGGCACAACACACA 435  
QY 122 AAAATGACACAGCAGGACCTATGCTTGATGGCCCCAGAG 164  
DB 496 CAAATGAGTCCCGCGGACCTACGCTGATGGATGCTCTGAGG 538  
RESULT 11  
LOCUS BQ227232 895 bp mRNA linear EST 02-MAY-2002  
DEFINITION AGENCOURT\_7567317 NIH\_MGC\_68 Homo sapiens cDNA clone IMAGE:6060488  
ACCESSION BQ227232  
VERSION BQ227232.1 GI:20408632  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 895)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: DCTD/DRP/Gazdar  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM13328 row: n column: 09  
High quality sequence stop: 673.  
FEATURES  
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Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6060488"  
/clone\_lib="NIH\_MGC\_68"  
/tissue\_type="large cell carcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: lung; Vector: PCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies."  
BASE COUNT 176 a 281 c 276 g 160 t 2 others  
ORIGIN  
Query Match 50.6%; Score 83; DB 14; Length 895;  
Best Local Similarity 69.3%; Pred. No. 2e-14;  
Matches 113; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
QY 2 CACCGGACATCAAGCAGGAATATTTGCTCTGAGAAGATGACATGACATC 61  
DB 242 CACCGGATCTCAAGTCCAAACATTTTCTCTGAGCCCATTTGAGATGACGACATG 301  
QY 62 TGCATATAAACTTTGAAGATTACAGATTTTGGTTGGCGAGGAGATGACAGACAC 121  
DB 302 GACGACAAAGACCTGAAGATCACGCACTTGGCTGGCCCGAAGTGGCACAACACACA 361  
QY 122 AAAATGACACAGCAGGACCTATGCTTGATGGCCCCAGAG 164  
DB 362 CAAATGAGTCCCGCGGACCTACGCTGATGGATGCTCTGAGG 404  
RESULT 12  
LOCUS BM549532 1057 bp mRNA linear EST 20-FEB-2002  
DEFINITION AGENCOURT\_6554238 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:5548665  
ACCESSION BM549532  
VERSION BM549532.1 GI:18785023  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1057)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: ATCC/DCTD/DRP  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
Plate: LLAM12257 row: p column: 10  
High quality sequence stop: 614.

## FEATURES

Location/Qualifiers  
1..1057

## source

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5548665"  
/clone\_1lb="NIH\_MGC\_72"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: PCMV-SPORE6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2 kb. Library constructed by life  
Technologies."

BASE COUNT 201 a 319 c 355 g 179 t 3 others  
ORIGIN

## Query Match

Best Local Similarity 50.6%; Score 83; DB 13; Length 1057;

Matches 113; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Db 2 CACCGGACATCAAGCAGAGAAATATTTGCTACTTGAGAGATGACATG 61

Db 371 CACCGATCTCAAGTCCAAACAACTTTGCTGCTGAGCCCATTTGAGTGAAGCATG 430

Db 62 TGCAATTAACCTTGAAGATTAAGATTTGGTGGGCGAGGAATGGCAGCAGACACC 121

Db 431 GAGCACAAGACCTGAGAGATCACCGACTTTGGCTGGCCCGAAGAGTGGCACAATACACA 490

QY 122 AAAATGACAGCAGCAGGACCTATGCTGTGATGGCCCGCAGAG 164

Db 491 CAATATGATGCGCGGCGACCTAGCCTGATGCTCTGAGG 533

## RESULT 13

## LOCUS

BQ709288 1278 bp mRNA linear EST 16-JUL-2002

DEFINITION AGENCOURT 7975607 NIH\_MGC\_113 Homo sapiens CDNA clone IMAGE:5215047

5', mRNA sequence.

ACCESSION BQ709288

VERSION BQ709288.1 GI:21848187

## KEYWORDS

EST.

## SOURCE

human.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1278)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2383 row: f column: 08

High quality sequence stop: 367.

Location/Qualifiers

1..1278

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5215047"

/clone\_1lb="NIH\_MGC\_113"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: spleen; Vector: pOTB7; Site\_1: XhoI; Site\_2:

EcoRI; CDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the

Laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

## BASE COUNT

280 a 375 c 419 g 200 t 4 others

## ORIGIN

## Query Match

Best Local Similarity 47.9%; Score 78.6; DB 14; Length 1278;

Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Db 8 GACATCAAGCAGGAATATTTGCTACTTGAGAGATGACATGACATTCGCAAT 67

Db 2 GATCTCAAGTCCAAACAACTTTGCTGCTGAGCCCATTTGAGAGTGAAGTGAAGCAGC 61

QY 68 AAAACTTGAAGATTAAGATTTGGTGGGCGAGGAATGGCAGCAGCAAAATG 127

Db 62 AAGACCTGAAGATCAAGCATTGCGCTGGCCGAGAGTGGCACAACCAACACCAATG 121

QY 128 AGCAGCAGCAGCAGCAGTATGCTGATGAGCCCGCAGAG 164

Db 122 AGTGGCGGCGGACCTAGCCCTGATGCTCTGAGG 158

## RESULT 14

## LOCUS

BG751808 863 bp mRNA linear EST 15-MAY-2001

DEFINITION 6027307451 NIH\_MGC\_43 Homo sapiens CDNA clone IMAGE:4874228 5',

mRNA sequence.

ACCESSION BG751808

VERSION BG751808.1 GI:14062461

## KEYWORDS

EST.

## SOURCE

human.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 863)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1753 row: j column: 11

High quality sequence stop: 856.

Location/Qualifiers

1..863

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4874218"

/clone\_1lb="NIH\_MGC\_43"

/tissue\_type="normal pigmented retinal epithelium"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: eye; Vector: pOTB7; Site\_1: XhoI; Site\_2:

EcoRI; CDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCAGCAG(G). Library constructed by Ling Hong

in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH\_MGC Library. "

## BASE COUNT

167 a 276 c 280 g 140 t

## ORIGIN

## Query Match

Best Local Similarity 45.9%; Score 75.2; DB 12; Length 863;

Matches 101; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| QY | 21  | GAAATATTTTGGTACTTGTAGAAAGATGAACATGATGACATCTGCATATTAACATTGTGAGA  | 80  |
|    | 1   | GCAAATATTTTGGTGTGTGAGCCCATTTGAGATGAGACATGTAGACACAAGACCTCTGAGA   | 60  |
| QY | 81  | TTACAGATTTTGGGTGTGGCGAGGGAAATGGACATGGACCAACCAATATGACACAGGAGCA   | 140 |
|    | 1   | TTACAGATTTTGGGTGTGGCGAGGGAAATGGACATGGACCAACCAATATGACACAGGAGCA   | 120 |
| Db | 61  | TCACCGACTTTGGCCTGTGGCCCGAGAGTGGCACAAATAACACACAAATGTAGTGGCGGGGCA | 120 |
| QY | 141 | CCATATGCTGGATGGGCCCCAGAA  | 164 |
|    | 121 | CCATATGCTGGATGGGCCCTCTGTAGG                                     | 144 |
| Db |     |   |     |

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OY      122  AAAATGACACACAGGACGACCTTACGCTGGATGGCCCCCAATG 164
          | | | | | | | | | | | | | | | | | | | | | |
Db      414  CAGATGATGCTGCGGGGACCTACGCTTGATGGATGCCACAG 456

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Search completed: December 13, 2002, 23:27:10  
 Job time : 2161 secs

Search completed: December 13, 2002, 23:27:10  
Job time : 2181 secs

|            |   |
|------------|---|
| RESULT     | 15  |
| BQ266193   |   |
| LOCUS      |   |
| DEFINITION | BQ266193 461 bp mRNA linear EST 07-MAY-2002   |
| ACCESION   | NJSC_ffile05.y1 NCL_CGAP_Mamms Mus musculus cDNA IMAGE:286512   |
| VERSION    | 5, mRNA sequence.   |
| KEYWORDS   | BQ266193..1 GI:20491258   |
| SOURCE     | EST.  |
| ORGANISM   | house mouse.  |
| TITLE      | Mus musculus  |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |
| AUTHORS    | Mammalia; Eutheria; Rodentia; Sclurognathii; Muridae; Murinae; Mus.   |
| TITLE      | 1 (bases 1 to 461)  |
| JOURNAL    | NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .  |
| COMMENT    | National Cancer Institute, Cancer Genome Anatomy Project (CGAP),<br>Tumor Gene Index<br>Unpublished (1997)<br>Contact: Robert Strausberg, Ph.D. |

Tissue Procurement: Lothar Hennighausen/Robin Humphreys  
 cDNA Library Preparation: Life Technologies  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNLN  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC)  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
[info@image.llnl.gov](mailto:info@image.llnl.gov)  
 MGI:1046284  
 Plate: L14W7069 row: J column: 9  
 Seq primer: M13NP1 reverse primer (ABI).  
 Location/Qualifiers  
     1..461

|                           |                                     |   |     |   |     |   |    |   |
|---------------------------|-------------------------------------|---|-----|---|-----|---|----|---|
| BASE COUNT                | 94                                  | a | 137 | c | 135 | g | 95 | t |
| ORIGIN                    |                                     |   |     |   |     |   |    |   |
| Query Match               | 45.7%; Score 75; DB 14; Length 461; |   |     |   |     |   |    |   |
| Best Local Similarity     | 66.3%; Pred. NO. 4,1e-12;           |   |     |   |     |   |    |   |
| Matches 108; Conservative | 0; Mismatches 55; Indels 0; Gaps 0; |   |     |   |     |   |    |   |

[illegible]